


protein-protein BLAST

Search

```

1pvvk1gnprkn1kpgevwaaigapigransvtagivsakgrs1pnesytpr1qtcavalnpg
nsggplfnlkggvginsqiyrsrggfmgisfaipidvamnvaeqlkntgkvqrgqlgvii
qevsyglagsfgldkasgaliakipgsphaeraglqagdivlsldgeirssgd1pvmvgai
tgcgkevslgvwrkgeeitikaklgnaehtgassktdeapteqqsgtfsvesagitlqth
tdssgkh1vvrvsdaaeraglrhgedilavrsprq

```

SEQ
ID NO: 4
U13881.80

Set subsequence From: [] To: []

Choose database **nr** []

Do CD-Search

Now: **BLAST!** or **Reset query** **Reset all**

Options for advanced blasting

Limit by entrez query [] or select from: (none) []

Composition-based statistics

Choose filter Low complexity Mask for lookup table only Mask lower case

Expect [10]

Word Size [3] []

Matrix **BLOSUM62** [] Gap Costs Existence: 11 Extension: 1 []

PSSM

Other advanced

PHL pattern

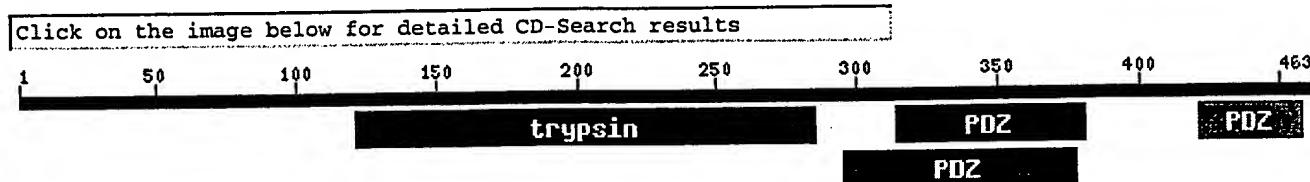


formatting BLAST

Your request has been successfully submitted and put into the Blast Queue.

Query = (463 letters)

Putative conserved domains have been detected



The request ID is **1002310688-22263-27915**

Format or **Reset all**

The results are estimated to be ready in 11 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show Graphical Overview NCBI-gi Alignment in **HTML** format

Number of: Descriptions **100** Alignments **50**

Alignment view **Pairwise**

Format for PSI-BLAST with inclusion threshold: **0.005**

Limit results by entrez query or select from:

Expect value range:

NCBI

CD-Search

Entrez ?

RPS-BLAST 2.2.1 [Apr-13-2001]

Query= (463 letters)

.. This CD alignment includes 3D structure. To display structure, download [Cn3D v3.00!](#)

Mouse-over boxes to display more information



PSSMs producing significant alignments:

		Score (bits)	E value
gnl Pfam pfam00089	trypsin, Trypsin. Proteins recognized include all proteins in ...	<u>68.6</u>	8e-13
gnl Smart smart00228	PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called D... PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called D...	<u>46.2</u>	4e-06
gnl Smart smart00228	PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called D...	<u>36.6</u>	0.003
gnl Pfam pfam00595	PDZ, PDZ domain (Also known as DHR or GLGF).. PDZ domains are ...	<u>40.4</u>	2e-04

[gnl|Pfam|pfam00089](#), trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*).

 Add query to multiple alignment, display up to 10 sequences most similar to the query

CD-Length = 217 residues, 89.9% aligned
Score = 68.6 bits (166), Expect = 8e-13

Query: 121	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLL-----NDKREYTAKLIGSDVQS--	171
Sbjct: 21	SSGHFCGGSLISEN-WVLTAACVSGASSVRVVLGEHNLGTTEQKFDVKKIIIVHPNY	79
Query: 172	-----DVALLKIDATEEL----PVVKIGNPKNLKPGE--WVAAGAPF--GFDNSVTAG	217
Sbjct: 80	NPDTNDIALLKLPVTLGDTVRPICLPSASSDLPVGTCVSGWGRTKNLGTSDTLQEV	139
Query: 218	IIVSAKGRSLPNESYTP-----FIQTD----VAINPGNSGGPLFNLIKQVVGINSQIYSRS	268
Sbjct: 140	VVPIVSRETCSRASGGTVDTMCAGALGGKDACPQGDGGPLVCSDELGVIVSWGYGCA	199
Query: 269	GGFMGISFAIPIDVAMN 285	
Sbjct: 200	VGN-YPGVYTRVSRYLD 215	

[gnl|Smart|smart00228](#), PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called DHR (Dlg homologous region) or GLGF (relatively well conserved tetrapeptide in these domains). Some PDZs have been shown to bind C-terminal polypeptides; others appear to bind internal (non-C-terminal) polypeptides. Different PDZs possess different binding specificities.

 query to multiple alignment, display sequences

CD-Length = 86 residues, only 79.1% aligned
Score = 46.2 bits (108), Expect = 4e-06

Query: 314	QSFGLDKASGALIAKI-PGSPAERAGLQAGDIVLSLDGGEIRSSGDLPVMVGAITPGKEV	372
Sbjct: 19	VGGKDSGDGGVVVSSVPGSPAAGLKGPDVILEVNGETSVEGLTHEAVDLLKEAGGKV	78
Query: 373	SLGVWRKG 380	
Sbjct: 79	TLTVLRGG 86	

- gnl|Smart|smart00228, PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called DHR (Dlg homologous region) or GLGF (relatively well conserved tetrapeptide in these domains). Some PDZs have been shown to bind C-terminal polypeptides; others appear to bind internal (non-C-terminal) polypeptides. Different PDZs possess different binding specificities.

Add query to multiple alignment, display up to 10 sequences most similar to the query

CD-Length = 86 residues, only 46.5% aligned
Score = 36.6 bits (83), Expect = 0.003

Query: 421 GITLQTHTDSSGKHLVVVRVSD--AAERAGLRHGDEILAV 458
Sbjct: 15 GFSLVGGKDSDGGVVVSSVPGSPAAGLKGPGDVILEV 54

gnl|Pfam|pfam00595, PDZ, PDZ domain (Also known as DHR or GLGF).. PDZ domains are found in diverse signaling proteins.

Add query to multiple alignment, display up to 10 sequences most similar to the query

CD-Length = 81 residues, 93.8% aligned
Score = 40.4 bits (93), Expect = 2e-04

Query: 295 KVQRGQLGVIIQEVSYGLAQSFGLDKASGALIAKI-PGSPAERAGLQAGDIVLSLDGGEI 353
Sbjct: 6 RQGRGGLGFSLKGGSQDKGDQ-----GIVVSEVLPGGAAERGGLKEGDRILEINGQDV 57

Query: 354 RSSGDLPMVGAITPGKEVSLGVW 377
Sbjct: 58 ENVTHERAVALALKSGCGEVTLTVL 81



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1: Rawlings ND, Barrett AJ.

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Methods Enzymol. 1994;244:19-61. No abstract available.

PMID: 7845208 [PubMed - indexed for MEDLINE]

2: Sprang S, Standing T, Fletterick RJ, Stroud RM, Finer-Moore J, Xuong NH, Hamlin R, Rutter WJ, Craik CS.

The three-dimensional structure of Asn102 mutant of trypsin: role of Asp102 in serine protease catalysis.

Science. 1987 Aug 21;237(4817):905-9.

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